

SEQUENCE LISTING

\* <110> Hua, Shao-bing  
Pauling, Michelle H.  
Zhu, Li

<120> HUMAN MONOCLONAL ANTIBODY AGAINST CORECEPTORS FOR HUMAN IMMUNODEFICIENCY VIRUS

<130> 25636-718

<160> 54

<170> PatentIn version 3.1

<210> 1  
<211> 352  
<212> PRT  
<213> Homo sapiens

<400> 1

Met Asp Tyr Gln Val Ser Ser Pro Ile Tyr Asp Ile Asn Tyr Tyr Thr  
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Ser Glu Pro Cys Gln Lys Ile Asn Val Lys Gln Ile Ala Ala Arg Leu  
20 25 30

Leu Pro Pro Leu Tyr Ser Leu Val Phe Ile Phe Gly Phe Val Gly Asn  
35 40 45

Met Leu Val Ile Leu Ile Leu Ile Asn Cys Lys Arg Leu Lys Ser Met  
50 55 60

Thr Asp Ile Tyr Leu Leu Asn Leu Ala Ile Ser Asp Leu Phe Phe Leu  
65 70 75 80

Leu Thr Val Pro Phe Trp Ala His Tyr Ala Ala Ala Gln Trp Asp Phe  
85 90 95

Gly Asn Thr Met Cys Gln Leu Leu Thr Gly Leu Tyr Phe Ile Gly Phe  
100 105 110

\* Phe Ser Gly Ile Phe Phe Ile Ile Leu Leu Thr Ile Asp Arg Tyr Leu  
115 120 125

Ala Val Val His Ala Val Phe Ala Leu Lys Ala Arg Thr Val Thr Phe  
130 135 140

Gly Val Val Thr Ser Val Ile Thr Trp Val Val Ala Val Phe Ala Ser  
145 150 155 160

Leu Pro Gly Ile Ile Phe Thr Arg Ser Gln Lys Glu Gly Leu His Tyr  
165 170 175

Thr Cys Ser Ser His Phe Pro Tyr Ser Gln Tyr Gln Phe Trp Lys Asn  
180 185 190

Phe Gln Thr Leu Lys Ile Val Ile Leu Gly Leu Val Leu Pro Leu Leu  
195 200 205

Val Met Val Ile Cys Tyr Ser Gly Ile Leu Lys Thr Leu Leu Arg Cys  
210 215 220

Arg Asn Glu Lys Lys Arg His Arg Ala Val Arg Leu Ile Phe Thr Ile  
225 230 235 240

Met Ile Val Tyr Phe Leu Phe Trp Ala Pro Tyr Asn Ile Val Leu Leu  
245 250 255

Leu Asn Thr Phe Gln Glu Phe Phe Gly Leu Asn Asn Cys Ser Ser Ser  
260 265 270

Asn Arg Leu Asp Gln Ala Met Gln Val Thr Glu Thr Leu Gly Met Thr  
275 280 285

His Cys Cys Ile Asn Pro Ile Ile Tyr Ala Phe Val Gly Glu Lys Phe  
290 295 300

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\* Arg Asn Tyr Leu Leu Val Phe Phe Gln Lys His Ile Ala Lys Arg Phe  
305 310 315 320

Cys Lys Cys Cys Ser Ile Phe Gln Gln Glu Ala Pro Glu Arg Ala Ser  
325 330 335

Ser Val Tyr Thr Arg Ser Thr Gly Glu Gln Glu Ile Ser Val Gly Leu  
340 345 350

<210> 2  
<211> 17  
<212> PRT  
<213> Homo sapiens

<400> 2

Gln Glu Phe Phe Gly Leu Asn Asn Cys Ser Ser Ser Asn Arg Leu Asp  
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Gln

<210> 3  
<211> 29  
<212> PRT  
<213> Homo sapiens

<400> 3

Glu Phe Phe Gly Leu Asn Asn Cys Ser Ser Ser Asn Arg Leu Asp Gln  
1 5 10 15

Ala Met Gln Val Thr Glu Thr Leu Gly Met Thr His Cys  
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<210> 4  
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<213> Artificial Sequence

<220>  
\* <223> G4S Linker

<400> 4

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1 5 10 15

Gly Gly Gly Ser  
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<210> 5  
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<220>  
\* <223> DNA of G4S Linker

<400> 5  
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<210> 6  
<211> 60  
<212> DNA  
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\* <223> 5' Homologous Sequence

<400> 6  
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<210> 7  
<211> 57  
<212> DNA  
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<220>  
\* <223> 3' Homologous Sequence

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<400> 7  
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57

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<211> 36  
<212> PRT  
<213> Homo sapiens

<400> 8

Met Asp Tyr Gln Val Ser Ser Pro Ile Tyr Asp Ile Asn Tyr Tyr Thr  
1 5 10 15

Ser Glu Pro Cys Gln Lys Ile Asn Val Lys Gln Ile Ala Ala Arg Leu  
20 25 30

Leu Pro Pro Leu  
35

<210> 9  
<211> 32  
<212> PRT  
<213> Homo sapiens

<400> 9

Thr Arg Ser Gln Lys Glu Gly Leu His Tyr Thr Cys Ser Ser His Phe  
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Pro Tyr Ser Gln Tyr Gln Phe Trp Lys Asn Phe Gln Thr Leu Lys Ile  
20 25 30

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<223> Primer  
  
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ggagaattcg attatcaagt gtcaagtcc  
30

<210> 11  
<211> 31  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Primer

<400> 11  
cgcggatcct tagagcgag gcaggaggcg g  
31

<210> 12  
<211> 29  
<212> DNA  
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<220>  
<223> Primer

<400> 12  
ggagaattca ccagatctca aaaagaagg  
29

<210> 13  
<211> 33  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Primer

<400> 13  
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33

<210> 14  
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<212> DNA  
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<220>  
<223> Primer  
  
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21  
  
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<223> Primer  
  
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31  
  
<210> 16  
<211> 759  
<212> DNA  
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<220>  
<223> Clone 15.186.35  
  
<400> 16  
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120  
  
cagccccag gaaaggccct tgagtggctt gcaagcataa attggaatga tgataagtgc  
180  
  
tacagccccat ctctgaaaag caggctcacc atcaccaagg acaccccaa aaaccaggta  
240  
  
gtccttgcaa tgagcaacat ggaccctgcg gacacagcca catattcctg tgcactcgat  
300  
  
atgccccccc atgatagtgg cccgcaatct tttgatgctt ctgatgtctg gggcccaggg  
360

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acaatggtca ccgtctttc aggccgtgggt ggatcaggcg gcggaggagtc tggcggaggt  
420

ggcagcggtg gtggaggcag ttcctatgag ctgatgcagc taccctcagt gtccgtgtcc  
480

ccaggacaga cagccagcat cacctgctct ggagataatt tggggataaa atatgcctgc  
540

tggtatcaac agaagccagg ccggccccct gtgctggtca tttatggaga taacaagcgg  
600

ccctcaggga tccctgagcg attctctggc tccaactctg ggaacacagc cactctgacc  
660

atcagcggga cccaggctat gnatgaggct gactattact gtcaggcgtg ggacaccagc  
720

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<210> 17

<211> 253

<212> PRT

<213> Artificial Sequence

<220>

<223> Clone 15.186.35

<400> 17

Gln Val Thr Leu Lys Glu Ser Gly Pro Thr Leu Val Lys Pro Thr Gln  
1 5 10 15

Thr Leu Thr Leu Thr Cys Thr Leu Ser Gly Phe Ser Leu Ser Thr Ser  
20 25 30

Gly Val Ser Val Gly Trp Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu  
35 40 45

Trp Leu Ala Ser Ile Asn Trp Asn Asp Asp Lys Cys Tyr Ser Pro Ser  
50 55 60

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Leu Lys Ser Arg Leu Thr Ile Thr Lys Asp Thr Pro Lys Asn Gln Val  
65 70 75 80

Val Leu Ala Met Ser Asn Met Asp Pro Ala Asp Thr Ala Thr Tyr Ser  
85 90 95

Cys Ala Leu Asp Met Pro Pro His Asp Ser Gly Pro Gln Ser Phe Asp  
100 105 110

Ala Ser Asp Val Trp Gly Pro Gly Thr Met Val Thr Val Ser Ser Gly  
115 120 125

Gly Gly Gly Ser Gly Gly Ser Gly Gly Gly Ser Gly Gly  
130 135 140

Gly Gly Ser Ser Tyr Glu Leu Met Gln Leu Pro Ser Val Ser Val Ser  
145 150 155 160

Pro Gly Gln Thr Ala Ser Ile Thr Cys Ser Gly Asp Asn Leu Gly Asp  
165 170 175

Lys Tyr Ala Cys Trp Tyr Gln Gln Lys Pro Gly Arg Ser Pro Val Leu  
180 185 190

Val Ile Tyr Gly Asp Asn Lys Arg Pro Ser Gly Ile Pro Glu Arg Phe  
195 200 205

Ser Gly Ser Asn Ser Gly Asn Thr Ala Thr Leu Thr Ile Ser Gly Thr  
210 215 220

Gln Ala Met Asp Glu Ala Asp Tyr Tyr Cys Gln Ala Trp Asp Thr Ser  
225 230 235 240

Thr Ala Val Phe Gly Thr Gly Thr Lys Leu Thr Val Leu  
245 250

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<210> 18  
<211> 762  
\* <212> DNA  
<213> Artificial Sequence  
  
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<223> Clone 15.150.11  
  
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120  
  
ccaggggagg gactggagtg gattggtttc atttcttcg atggagcac caactacaac  
180  
  
ccctccctca acggtcgagt caccatctca ctcgacacgt cgaagaatca gctctccctg  
240  
  
aggctgacct ctgtgaccgc tgccggacacg gccgtgtatt tctgtgcgag actaaagggg  
300  
  
gcgtggttat tgtctgaacc cccttacttc agctccgacg gcatggacgt ctggggccaa  
360  
  
gggaccacgg tcaccgtccc ctcaggcggt ggtggatcag gcccggagg atctggcgg  
420  
  
ggtggcagcg gtggggagg cagtaattt atgctgactc agccccctc agcgtctgg  
480  
  
accccccggc agagggtcag catctttgt tctggagca gctccgacat cgaaagtaat  
540  
  
actgtaaact ggtaccagca actcccagga acggcccca aactcctcat ctatagtaat  
600  
  
aatcagcggc cctcaggggt ccctgaccga ttctctggct tcaagtctgg cacctcagcc  
660  
  
tccctggta tcaagtggcct ccagtctgag gatgaggctg attattattg tgcagcatgg  
720  
  
gatgagagcc tgaatggtgt ggtgttcggc ggaggacaa gg  
762

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\* <210> 19  
\* <211> 254  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Clone 15.150.11

<400> 19

1 Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu  
5 10 15

20 Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Gly His Asp  
25 30

35 Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Glu Gly Leu Glu Trp Ile  
40 45

50 Gly Phe Ile Phe Phe Asp Gly Ser Thr Asn Tyr Asn Pro Ser Leu Asn  
55 60

65 Gly Arg Val Thr Ile Ser Leu Asp Thr Ser Lys Asn Gln Leu Ser Leu  
70 75 80

85 Arg Leu Thr Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Phe Cys Ala  
90 95

100 Arg Leu Lys Gly Ala Trp Leu Leu Ser Glu Pro Pro Tyr Phe Ser Ser  
105 110

115 Asp Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Pro Ser  
120 125

130 Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly  
135 140

Gly Gly Gly Ser Asn Phe Met Leu Thr Gln Pro Pro Ser Ala Ser Gly

Genetastix.718.ST25

145 150 155 160

Thr Pro Gly Gln Arg Val Ser Ile Ser Cys Ser Gly Ser Ser Ser Asp  
165 170 175

Ile Gly Ser Asn Thr Val Asn Trp Tyr Gln Gln Leu Pro Gly Thr Ala  
180 185 190

Pro Lys Leu Leu Ile Tyr Ser Asn Asn Gln Arg Pro Ser Gly Val Pro  
195 200 205

Asp Arg Phe Ser Gly Phe Lys Ser Gly Thr Ser Ala Ser Leu Val Ile  
210 215 220

Ser Gly Leu Gln Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Ala Trp  
225 230 235 240

Asp Glu Ser Leu Asn Gly Val Val Phe Gly Gly Gly Pro Arg  
245 250

<210> 20  
<211> 750  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Clone 15.150.12

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120  
ccagggaagg ggctggagtg gattggggag atcaatcatc gtggaagcac tacctacaac  
180  
ccgtccctcg acggtcgagt caccatatca ttagacacat ctaccaacca gatctccctt  
240

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aaactgacct ctatgaccgc cgccggacacg gccgtgtatt actgtgcgag gacagtggct  
300

ggtactagtg actactgggg ccagggAACc ctggtcaccc tttcctcagg gagtgcatcc  
360

gcccccaacgg gcgggtggtgg atcaggcggc ggaggatctg gcggaggtgg cagcgggtgg  
420

ggaggcagta aaacgacact cacgcagtct ccagcattca tgcagcgac tccaggagac  
480

aaagtcagca ttcctgcaa agccagccga gacgttgatg atgatgtgaa ctggtaacaa  
540

cagagaccag gagaagctcc tattttcatt attgaagatg ctactactct cgttcctgg  
600

atctcacctc gattcagtgg cagcgggtat ggaaccgatt ttaccctcac aattaataac  
660

atcgattctg aggatgctgc atattatttc tgtctacaac atgataattt cccgctcacc  
720

ttcggccggag ggaccaaggt ggagatcaaa  
750

<210> 21  
<211> 250  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Clone 15.150.12

<400> 21

Gln Val Gln Leu Gln Gln Trp Gly Ala Gly Leu Leu Lys Ser Trp Gly  
1 5 10 15

Thr Leu Ser Leu Thr Cys Ala Val Ser Gly Ala Ser Phe Ser Gly Tyr  
20 25 30

Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile  
35 40 45

\* Gly Glu Ile Asn His Arg Gly Ser Thr Thr Tyr Asn Pro Ser Leu Asp  
50 55 60

Gly Arg Val Thr Ile Ser Leu Asp Thr Ser Thr Asn Gln Ile Ser Leu  
65 70 75 80

Lys Leu Thr Ser Met Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala  
85 90 95

\* Arg Thr Val Ala Gly Thr Ser Asp Tyr Trp Gly Gln Gly Thr Leu Val  
100 105 110

Thr Val Ser Ser Gly Ser Ala Ser Ala Pro Thr Gly Gly Gly Ser  
115 120 125

\* Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Lys  
130 135 140

\* Thr Thr Leu Thr Gln Ser Pro Ala Phe Met Ser Ala Thr Pro Gly Asp  
145 150 155 160

Lys Val Ser Ile Ser Cys Lys Ala Ser Arg Asp Val Asp Asp Asp Val  
165 170 175

Asn Trp Tyr Gln Gln Arg Pro Gly Glu Ala Pro Ile Phe Ile Ile Glu  
180 185 190

Asp Ala Thr Thr Leu Val Pro Gly Ile Ser Pro Arg Phe Ser Gly Ser  
195 200 205

Gly Tyr Gly Thr Asp Phe Thr Leu Thr Ile Asn Asn Ile Asp Ser Glu  
210 215 220

Asp Ala Ala Tyr Tyr Phe Cys Leu Gln His Asp Asn Phe Pro Leu Thr  
225 230 235 240

\* Phe Gly Gly Gly Thr Lys Val Glu Ile Lys  
245 250

<210> 22  
<211> 759  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Clone 15.150.24

<400> 22  
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120  
cagccccccag gaaaggccct ggaatggcct gcactcattt attgggatga tgataagcgc  
180  
tacagccccat ctctgaagag caggctcacc atcaccaagg acacctccaa aaagcaggtg  
240  
gtccttacaa tgaccaacgt ggacccagcg gacacagccca cctattactg tacacacgag  
300  
caataactatt atgataactag tggtcagcca tactactttg acttctgggg ccagggcacc  
360  
ctggtcacccg tctcctcagg cggtggtgga tcaggcggcg gaggatctgg cggaggtggc  
420  
agcgggtggtg gaggcagtaa catccaggtg acccagtctc catcctccct gtctgcattct  
480  
gttaggagaca gagtcaccat gacttgcggg gcgagtcagg acattaggaa gaatttaaat  
540  
tggtatcagc aaaaaccagg gaaaggccct aaggtcctga tctacgatgc atccgatttg  
600  
gaaacagggta tcccatcaag gttcagtgga agtggatctg ggacagattt tatcctcacc  
660

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atcagcagcc tgcagcctga agatattgca acatactact gtcaacagtc tgattattta  
720

ccgctcactt tcggcggagg gaccaaagtg gatatcaaa  
759

<210> 23  
<211> 253  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Clone 15.150.24

<400> 23

Gln Val Thr Leu Lys Glu Ser Gly Pro Thr Leu Val Lys Pro Thr Gln  
1 5 10 15

Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Arg Thr Thr  
20 25 30

Gly Glu Gly Val Gly Trp Val Arg Gln Pro Pro Gly Lys Ala Leu Glu  
35 40 45

Trp Leu Ala Leu Ile Tyr Trp Asp Asp Asp Lys Arg Tyr Ser Pro Ser  
50 55 60

Leu Lys Ser Arg Leu Thr Ile Thr Lys Asp Thr Ser Lys Lys Gln Val  
65 70 75 80

Val Leu Thr Met Thr Asn Val Asp Pro Ala Asp Thr Ala Thr Tyr Tyr  
85 90 95

Cys Thr His Glu Gln Tyr Tyr Asp Thr Ser Gly Gln Pro Tyr Tyr  
100 105 110

Phe Asp Phe Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly  
115 120 125

Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly  
130 135 140

Gly Ser Asn Ile Gln Val Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser  
145 150 155 160

Val Gly Asp Arg Val Thr Met Thr Cys Arg Ala Ser Gln Asp Ile Arg  
165 170 175

Lys Asn Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Val  
180 185 190

Leu Ile Tyr Asp Ala Ser Asp Leu Glu Thr Gly Ile Pro Ser Arg Phe  
195 200 205

Ser Gly Ser Gly Ser Gly Thr Asp Phe Ile Leu Thr Ile Ser Ser Leu  
210 215 220

Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Ser Asp Tyr Leu  
225 230 235 240

Pro Leu Thr Phe Gly Gly Thr Lys Val Asp Ile Lys  
245 250

<210> 24

<211> 759

<212> DNA

<213> Artificial Sequence

<220>

<223> Clone 15.186.35 Variant

<400> 24

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acacctgcaccc tgtctgggtt ctcactcagc actagtgag tgagtgtggg ctggatccgt  
120

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cagccccca gaaaggccct tgagtggctt gcaagcataa attggaatga tgataagtgc  
180  
tacagcccat ctctgaaaag caggctcacc atcaccaagg acaccccaa aaaccaggtg  
240  
gtccttgcaa tgagcaacat ggaccctgcg gacacagcca catattcctg tgcactcgat  
300  
atgccccccc atgatagtgg cccgcaatct tttgatgctt ctgatgtctg gggcccaggg  
360  
acaatggtca ccgtctttc aggccgtgg gatcaggcg gcggaggatc tggcggaggt  
420  
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480  
ccaggacaga cagccagcat cacctgctct ggagataatt tggggataaa atatgcctgc  
540  
tggtatcaac agaagccagg ccggccccct gtgctggtca tttatggaga taacaagcgg  
600  
ccctcaggga tccctgagcg attctctggc tccaaactctg ggaacacagc cactctgacc  
660  
atcagccgga cccaggctat ggatgaggct gactattact gtcaggcgtg ggacaccagc  
720  
actgctgtct tcggaactgg gaccaagctc accgtccta  
759

<210> 25  
<211> 253  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Clone 15.186.35 Variant

<400> 25

Gln Val Thr Leu Lys Glu Ser Gly Pro Thr Leu Val Lys Pro Thr Gln  
1 5 10 15

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Thr Leu Thr Leu Thr Cys Thr Leu Ser Gly Phe Ser Leu Ser Thr Ser  
20 25 30

Gly Val Ser Val Gly Trp Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu  
35 40 45

Trp Leu Ala Ser Ile Asn Trp Asn Asp Asp Lys Cys Tyr Ser Pro Ser  
50 55 60

Leu Lys Ser Arg Leu Thr Ile Thr Lys Asp Thr Pro Lys Asn Gln Val  
65 70 75 80

Val Leu Ala Met Ser Asn Met Asp Pro Ala Asp Thr Ala Thr Tyr Ser  
85 90 95

Cys Ala Leu Asp Met Pro Pro His Asp Ser Gly Pro Gln Ser Phe Asp  
100 105 110

Ala Ser Asp Val Trp Gly Pro Gly Thr Met Val Thr Val Ser Ser Gly  
115 120 125

Gly Gly Gly Ser Gly Gly Ser Gly Gly Gly Ser Gly Gly  
130 135 140

Gly Gly Ser Ser Tyr Glu Leu Met Gln Leu Pro Ser Val Ser Val Ser  
145 150 155 160

Pro Gly Gln Thr Ala Ser Ile Thr Cys Ser Gly Asp Asn Leu Gly Asp  
165 170 175

Lys Tyr Ala Cys Trp Tyr Gln Gln Lys Pro Gly Arg Ser Pro Val Leu  
180 185 190

Val Ile Tyr Gly Asp Asn Lys Arg Pro Ser Gly Ile Pro Glu Arg Phe  
195 200 205

Ser Gly Ser Asn Ser Gly Asn Thr Ala Thr Leu Thr Ile Ser Gly Thr  
210 215 220

Gln Ala Met Asp Glu Ala Asp Tyr Tyr Cys Gln Ala Trp Asp Thr Ser  
225 230 235 240

Thr Ala Val Phe Gly Thr Gly Thr Lys Leu Thr Val Leu  
245 250

<210> 26

<211> 774

<212> DNA

<213> Artificial Sequence

<220>

<223> Clone 15.150.11 Variant

<400> 26

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acttgactg tctctggtgg ctccatcggt catgactact ggagctggat acggcagccc  
120

ccaggggagg gactggagtg gattggtttc atcttcttcg atgggagcac caactacaac  
180

ccctccctca acggtcgagt caccatctca ctcgacacgt cgaagaatca gctctccctg  
240

aggctgacct ctgtgaccgc tgcggacacg gccgtgtatt tctgtgcgag actaaagggg  
300

gcgtggttat tgtctgaacc cccttacttc agctccgacg gcatggacgt ctggggccaa  
360

gggaccacgg tcaccgtctc ctcaggcggt ggtggatcag gcggcggagg atctggcgg  
420

ggtggcagcg gtggtgagg cagtaatttt atgctgactc agccccccctc agcgtctgg  
480

accccccgggc agagggtcag catctttgt tctggagca gctccgacat cggaagtaat  
540

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actgtaaact ggtaccagca actcccagga acggccccc aactcctcat ctatagtaat  
600

aatcagcggc cctcaggggt ccctgaccga ttctctggct tcaagtctgg cacctcagcc  
660

tccctggtca tcagtggcct ccagtctgag gatgaggctg attattattg tgcagcatgg  
720

gatgagagcc tgaatggtgt ggtgttcggc ggaggaacca aggtgaccgt ccta  
774

<210> 27

<211> 258

<212> PRT

<213> Artificial Sequence

<220>

<223> Clone 15.150.11

<400> 27

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu  
1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Gly His Asp  
20 25 30

Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Glu Gly Leu Glu Trp Ile  
35 40 45

Gly Phe Ile Phe Phe Asp Gly Ser Thr Asn Tyr Asn Pro Ser Leu Asn  
50 55 60

Gly Arg Val Thr Ile Ser Leu Asp Thr Ser Lys Asn Gln Leu Ser Leu  
65 70 75 80

Arg Leu Thr Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Phe Cys Ala  
85 90 95

Arg Leu Lys Gly Ala Trp Leu Leu Ser Glu Pro Pro Tyr Phe Ser Ser

Genetastix.718.ST25

100

105

110

Asp Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser  
115 120 125

Gly Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly  
130 135 140

Gly Gly Gly Ser Asn Phe Met Leu Thr Gln Pro Pro Ser Ala Ser Gly  
145 150 155 160

Thr Pro Gly Gln Arg Val Ser Ile Ser Cys Ser Gly Ser Ser Ser Asp  
165 170 175

Ile Gly Ser Asn Thr Val Asn Trp Tyr Gln Gln Leu Pro Gly Thr Ala  
180 185 190

Pro Lys Leu Leu Ile Tyr Ser Asn Asn Gln Arg Pro Ser Gly Val Pro  
195 200 205

Asp Arg Phe Ser Gly Phe Lys Ser Gly Thr Ser Ala Ser Leu Val Ile  
210 215 220

Ser Gly Leu Gln Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Ala Trp  
225 230 235 240

Asp Glu Ser Leu Asn Gly Val Val Phe Gly Gly Gly Thr Lys Val Thr  
245 250 255

Val Leu

<210> 28  
<211> 750  
<212> DNA  
<213> Artificial Sequence

Genetastix.718.ST25

<220>  
<223> Clone 15.150.12 Variant

<400> 28  
caggtgcagc tacagcagtg gggcgccagga ctgttgaagt cttggggAAC cctgtccctc  
60  
acctgcgctg tctctggtgc gtcgttttagt ggttattttt ggagctggat ccgccagccc  
120  
ccagggaagg ggctggagtg gattggggag atcaatcatc gtggaaAGCAC tacctacaac  
180  
ccgtccctcg acggtcgagt caccatatca ttagacacat ctaccaacca gatctccctt  
240  
aaactgacct ctatgaccgc cgccggacacg gccgtgtatt actgtgcgag gacagtggct  
300  
ggtactagtg actactgggg ccagggaacc ctggtcacccg tttcctcagg gagtgcaccc  
360  
cccccaacgg gcgggtggg atcaggcggc ggaggatctg gcggaggtgg cagcgggtgg  
420  
ggaggcagtg aaacgacact cacgcagttt ccagcattca tgtcagcgac tccaggagac  
480  
aaagtcaGca tctcctgcaa agccagccga gacgttGatg atgatgtgaa ctggtaGcaa  
540  
cagagaccag gagaagctcc tattttcatt attgaagatg ctactactct cgttcctgga  
600  
atctcacctc gattcagtgg cagcggtat ggaaccgatt ttaccctcac aattaataac  
660  
atcgattctg aggatgctgc atattatttc tgtctacaac atgataattt cccgctcacc  
720  
ttcggcggag ggaccaaggt ggagatcaaa  
750

<210> 29  
<211> 250  
<212> PRT  
<213> Artificial Sequence

Genetastix.718.ST25

\* <220>

\* <223> Clone 15.150.12 Variant

<400> 29

Gln Val Gln Leu Gln Gln Trp Gly Ala Gly Leu Leu Lys Ser Trp Gly  
1 5 10 15

Thr Leu Ser Leu Thr Cys Ala Val Ser Gly Ala Ser Phe Ser Gly Tyr  
20 25 30

Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile  
35 40 45

Gly Glu Ile Asn His Arg Gly Ser Thr Thr Tyr Asn Pro Ser Leu Asp  
50 55 60

Gly Arg Val Thr Ile Ser Leu Asp Thr Ser Thr Asn Gln Ile Ser Leu  
65 70 75 80

Lys Leu Thr Ser Met Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala  
85 90 95

Arg Thr Val Ala Gly Thr Ser Asp Tyr Trp Gly Gln Gly Thr Leu Val  
100 105 110

Thr Val Ser Ser Gly Ser Ala Ser Ala Pro Thr Gly Gly Gly Ser  
115 120 125

Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Glu  
130 135 140

Thr Thr Leu Thr Gln Ser Pro Ala Phe Met Ser Ala Thr Pro Gly Asp  
145 150 155 160

Lys Val Ser Ile Ser Cys Lys Ala Ser Arg Asp Val Asp Asp Asp Val  
165 170 175

\* Asn Trp Tyr Gln Gln Arg Pro Gly Glu Ala Pro Ile Phe Ile Ile Glu  
180 185 190

Asp Ala Thr Thr Leu Val Pro Gly Ile Ser Pro Arg Phe Ser Gly Ser  
195 200 205

Gly Tyr Gly Thr Asp Phe Thr Leu Thr Ile Asn Asn Ile Asp Ser Glu  
210 215 220

Asp Ala Ala Tyr Tyr Phe Cys Leu Gln His Asp Asn Phe Pro Leu Thr  
225 230 235 240

Phe Gly Gly Gly Thr Lys Val Glu Ile Lys  
245 250

<210> 30  
<211> 759  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Clone 15.150.24 Variant

<400> 30  
caggtcacct tgaaggagtc tggtcctacg ctggtgaaac ccacacagac cctcacgctg  
60

acctgcaccc tctctgggtt ctcactcaga actactggag agggtgtggg ctgggtccgt  
120

cagccccccag gaaaggccct ggaatggctt gcactcattt attgggatga tgataagcgc  
180

tacagcccat ctctgaagag caggctcacc atcaccagg acacctccaa aaagcagggtg  
240

gtccttacaa tgaccaacgt ggaccagcg gacacagcca cctattactg tacacacgag  
300

caataactatt atgataactag tggtcagcca tactactttg acttctgggg ccagggcacc  
360

ctggtcaccg tctcctcagg cggtggtgga tcagggcgcg gaggatctgg cggaggtggc  
420

agcggtggtg gaggcagtaa catccaggtg acccagtctc catcctccct gtctgcacatct  
480

gtaggagaca gagtcaccat gacttgccgg gcgagtcagg acattaggaa gaatttaaat  
540

tggtatcagc aaaaaccagg gaaagccct aaggtcctga tctacgatgc atccgatttg  
600

gaaacaggga tcccatcaag gttcagtggaa agtggatctg ggacagattt tatcctcacc  
660

atcagcagcc tgcagcctga agatattgca acatactact gtcaacagtc tgattattta  
720

ccgctcaatt tggcggagg gaccaaagtg gatataaaa  
759

<210> 31

<211> 253

<212> PRT

<213> Artificial Sequence

<220>

<223> Clone 15.150.24 Variant

<400> 31

Gln Val Thr Leu Lys Glu Ser Gly Pro Thr Leu Val Lys Pro Thr Gln  
1 5 10 15

Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Arg Thr Thr  
20 25 30

Gly Glu Gly Val Gly Trp Val Arg Gln Pro Pro Gly Lys Ala Leu Glu  
35 40 45

Trp Leu Ala Leu Ile Tyr Trp Asp Asp Asp Lys Arg Tyr Ser Pro Ser  
50 55 60

Genetastix.718.ST25

Leu Lys Ser Arg Leu Thr Ile Thr Lys Asp Thr Ser Lys Lys Gln Val  
65 70 75 80

Val Leu Thr Met Thr Asn Val Asp Pro Ala Asp Thr Ala Thr Tyr Tyr  
85 90 95

Cys Thr His Glu Gln Tyr Tyr Asp Thr Ser Gly Gln Pro Tyr Tyr  
100 105 110

Phe Asp Phe Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly  
115 120 125

Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly  
130 135 140

Gly Ser Asn Ile Gln Val Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser  
145 150 155 160

Val Gly Asp Arg Val Thr Met Thr Cys Arg Ala Ser Gln Asp Ile Arg  
165 170 175

Lys Asn Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Val  
180 185 190

Leu Ile Tyr Asp Ala Ser Asp Leu Glu Thr Gly Ile Pro Ser Arg Phe  
195 200 205

Ser Gly Ser Gly Ser Gly Thr Asp Phe Ile Leu Thr Ile Ser Ser Leu  
210 215 220

Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Ser Asp Tyr Leu  
225 230 235 240

Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Asp Ile Lys  
245 250

\* <210> 32  
<211> 9  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> VH CDR2

<220>  
<221> MISC\_FEATURE  
<222> (4)..(4)  
<223> X = Asparagine or Threonine

400 <400> 32

Gly Ser Thr Xaa Tyr Asn Pro Ser Leu  
1 5

\* <210> 33  
<211> 5  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> VL CDR2

<220>  
<221> MISC\_FEATURE  
<222> (3)..(4)  
<223> X3 = Asparagine or Threonine  
X4 = Threonine or Aspartic acid

<400> 33

Asp Ala Xaa Xaa Leu  
1 5

<210> 34  
<211> 127  
<212> PRT  
<213> Homo sapiens

<400> 34

Genetastix.718.ST25

Gln Val Thr Leu Lys Glu Ser Gly Pro Thr Leu Val Lys Pro Thr Gln  
1 5 10 15

Thr Leu Thr Leu Thr Cys Thr Leu Ser Gly Phe Ser Leu Ser Thr Ser  
20 25 30

Gly Val Ser Val Gly Trp Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu  
35 40 45

Trp Leu Ala Ser Ile Asn Trp Asn Asp Asp Lys Cys Tyr Ser Pro Ser  
50 55 60

Leu Lys Ser Arg Leu Thr Ile Thr Lys Asp Thr Pro Lys Asn Gln Val  
65 70 75 80

Val Leu Ala Met Ser Asn Met Asp Pro Ala Asp Thr Ala Thr Tyr Ser  
85 90 95

Cys Ala Leu Asp Met Pro Pro His Asp Ser Gly Pro Gln Ser Phe Asp  
100 105 110

Ala Ser Asp Val Trp Gly Pro Gly Thr Met Val Thr Val Ser Ser  
115 120 125

<210> 35  
<211> 106  
<212> PRT  
<213> Homo sapiens

<400> 35

Ser Tyr Glu Leu Met Gln Leu Pro Ser Val Ser Val Ser Pro Gly Gln  
1 5 10 15

Thr Ala Ser Ile Thr Cys Ser Gly Asp Asn Leu Gly Asp Lys Tyr Ala  
20 25 30

Genetastix.718.ST25

Cys Trp Tyr Gln Gln Lys Pro Gly Arg Ser Pro Val Leu Val Ile Tyr  
35 40 45

Gly Asp Asn Lys Arg Pro Ser Gly Ile Pro Glu Arg Phe Ser Gly Ser  
50 55 60

Asn Ser Gly Asn Thr Ala Thr Leu Thr Ile Ser Gly Thr Gln Ala Met  
65 70 75 80

Asp Glu Ala Asp Tyr Tyr Cys Gln Ala Trp Asp Thr Ser Thr Ala Val  
85 90 95

Phe Gly Thr Gly Thr Lys Leu Thr Val Leu  
100 105

<210> 36  
<211> 126  
<212> PRT  
<213> Homo sapiens

<400> 36

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu  
1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Gly His Asp  
20 25 30

Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Glu Gly Leu Glu Trp Ile  
35 40 45

Gly Phe Ile Phe Phe Asp Gly Ser Thr Asn Tyr Asn Pro Ser Leu Asn  
50 55 60

Gly Arg Val Thr Ile Ser Leu Asp Thr Ser Lys Asn Gln Leu Ser Leu  
65 70 75 80

Arg Leu Thr Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Phe Cys Ala

Genetastix.718.ST25

85

90

95

Arg Leu Lys Gly Ala Trp Leu Leu Ser Glu Pro Pro Tyr Phe Ser Ser  
100 105 110

Asp Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val  
115 120 125

<210> 37

<211> 104

<212> PRT

<213> Homo sapiens

<400> 37

Asn Phe Met Leu Thr Gln Pro Pro Ser Ala Ser Gly Thr Pro Gly Gln  
1 5 10 15

Arg Val Ser Ile Ser Cys Ser Gly Ser Ser Ser Asp Ile Gly Ser Asn  
20 25 30

Thr Val Asn Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu Leu  
35 40 45

Ile Tyr Ser Asn Asn Gln Arg Pro Ser Gly Val Pro Asp Arg Phe Ser  
50 55 60

Gly Phe Lys Ser Gly Thr Ser Ala Ser Leu Val Ile Ser Gly Leu Gln  
65 70 75 80

Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Ala Trp Asp Glu Ser Leu  
85 90 95

Asn Gly Val Val Phe Gly Gly  
100

<210> 38

<211> 116

Genetastix.718.ST25

> <212> PRT

> <213> Homo sapiens

> <400> 38

Gln Val Gln Leu Gln Gln Trp Gly Ala Gly Leu Leu Lys Ser Trp Gly  
1 5 10 15

Thr Leu Ser Leu Thr Cys Ala Val Ser Gly Ala Ser Phe Ser Gly Tyr  
20 25 30

Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile  
35 40 45

Gly Glu Ile Asn His Arg Gly Ser Thr Thr Tyr Asn Pro Ser Leu Asp  
50 55 60

Gly Arg Val Thr Ile Ser Leu Asp Thr Ser Thr Asn Gln Ile Ser Leu  
65 70 75 80

Lys Leu Thr Ser Met Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala  
85 90 95

Arg Thr Val Ala Gly Thr Ser Asp Tyr Trp Gly Gln Gly Thr Leu Val  
100 105 110

Thr Val Ser Ser  
115

<210> 39

<211> 106

<212> PRT

<213> Homo sapiens

<400> 39

Thr Thr Leu Thr Gln Ser Pro Ala Phe Met Ser Ala Thr Pro Gly Asp  
1 5 10 15

Genetastix.718.ST25

Lys Val Ser Ile Ser Cys Lys Ala Ser Arg Asp Val Asp Asp Asp Val  
20 25 30

Asn Trp Tyr Gln Gln Arg Pro Gly Glu Ala Pro Ile Phe Ile Ile Glu  
35 40 45

Asp Ala Thr Thr Leu Val Pro Gly Ile Ser Pro Arg Phe Ser Gly Ser  
50 55 60

Gly Tyr Gly Thr Asp Phe Thr Leu Thr Ile Asn Asn Ile Asp Ser Glu  
65 70 75 80

Asp Ala Ala Tyr Tyr Phe Cys Leu Gln His Asp Asn Phe Pro Leu Thr  
85 90 95

Phe Gly Gly Thr Lys Val Glu Ile Lys  
100 105

<210> 40

<211> 126

<212> PRT

<213> Homo sapiens

<400> 40

Gln Val Thr Leu Lys Glu Ser Gly Pro Thr Leu Val Lys Pro Thr Gln  
1 5 10 15

Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Arg Thr Thr  
20 25 30

Gly Glu Gly Val Gly Trp Val Arg Gln Pro Pro Gly Lys Ala Leu Glu  
35 40 45

Trp Leu Ala Leu Ile Tyr Trp Asp Asp Asp Lys Arg Tyr Ser Pro Ser  
50 55 60

Leu Lys Ser Arg Leu Thr Ile Thr Lys Asp Thr Ser Lys Lys Gln Val

Genetastix.718.ST25

65

70

75

80

Val Leu Thr Met Thr Asn Val Asp Pro Ala Asp Thr Ala Thr Tyr Tyr  
85 90 95

Cys Thr His Glu Gln Tyr Tyr Asp Thr Ser Gly Gln Pro Tyr Tyr  
100 105 110

Phe Asp Phe Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser  
115 120 125

<210> 41

<211> 107

<212> PRT

<213> Homo sapiens

<400> 41

Asn Ile Gln Val Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly  
1 5 10 15

Asp Arg Val Thr Met Thr Cys Arg Ala Ser Gln Asp Ile Arg Lys Asn  
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Val Leu Ile  
35 40 45

Tyr Asp Ala Ser Asp Leu Glu Thr Gly Ile Pro Ser Arg Phe Ser Gly  
50 55 60

Ser Gly Ser Gly Thr Asp Phe Ile Leu Thr Ile Ser Ser Leu Gln Pro  
65 70 75 80

Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Ser Asp Tyr Leu Pro Leu  
85 90 95

Thr Phe Gly Gly Thr Lys Val Asp Ile Lys  
100 105

\* <210> 42  
<211> 5  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Linker Sequence

<400> 42

Gly Gly Gly Gly Ser  
1 5

<210> 43  
<211> 21  
<212> PRT  
<213> Homo sapiens

<400> 43

Arg Leu Lys Gly Ala Trp Leu Leu Ser Glu Pro Pro Tyr Phe Ser Ser  
1 5 10 15

Asp Gly Met Asp Val  
20

<210> 44  
<211> 9  
<212> PRT  
<213> Homo sapiens

<400> 44

Arg Thr Val Ala Gly Thr Ser Asp Tyr  
1 5

<210> 45  
<211> 17  
<212> PRT  
<213> Homo sapiens

<400> 45

His Glu Gln Tyr Tyr Asp Thr Ser Gly Gln Pro Tyr Tyr Phe Asp  
1 5 10 15

Phe

<210> 46  
<211> 11  
<212> PRT  
<213> Homo sapiens

<400> 46

Ala Ala Trp Asp Glu Ser Leu Asn Gly Val Val  
5 10

<210> 47  
<211> 9  
<212> PRT  
<213> Homo sapiens

<400> 47

Leu Gln His Asp Asn Phe Pro Leu Thr  
1 5

<210> 48  
<211> 9  
<212> PRT  
<213> Homo sapiens

<400> 48

Gln Gln Ser Asp Tyr Leu Pro Leu Thr  
1 5

<210> 49  
<211> 30  
<212> DNA  
<213> Artificial Sequence

<220>

<223> Primer

\* <400> 49  
ggagaattcg attatcaagt gtcaagtcca  
30

<210> 50

<211> 31

<212> DNA

<213> Artificial Sequence

<220>

\* <223> Primer

\* <400> 50  
cgccggatcct tagagcggag gcaggaggcg g  
31

\* <210> 51

\* <211> 29

\* <212> DNA

\* <213> Artificial Sequence

\* <220>

\* <223> Primer

<400> 51

ggagaattca ccagatctca aaaagaagg

29

<210> 52

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 52

cgcggatcct tatatcttta atgtctggaa att  
33

<210> 53

<211> 21

<212> DNA  
<213> Artificial Sequence

<220>  
<223> Primer

<400> 53  
caggaattct ttggcctgaa t  
21

<210> 54  
<211> 31  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Primer

<400> 54  
cgccgatcct cagcagtgcg tcatcccaag a  
31